



SEQUENCE LISTING

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<120> GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

<130> 5051.458IP

<140> US 10/633,850

<141> 2003-08-04

<150> US 09/289,346

<151> 1999-04-09

<150> US 60/125,004

<151> 1999-03-18

<160> 113

<170> PatentIn version 3.3

<210> 1

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Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
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 <223> Wild-type TGMV AL1 amino acids 111-180

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Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
 35 40 45

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 50 55 60

Asp Lys Thr Pro Glu Pro
 65 70

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 <223> RS-R125 (Ala1) mutation

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 20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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<223> E--N140 + KEE146 (Ala4+5) mutation

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Ser Ala Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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<223> REK154 (Ala6) mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
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Ser Lys Glu Glu Ala Leu Gln Ile Ile Ala Ala Ala Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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<223> EKY159 (Ala7) mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala
35 40 45

Ala Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe

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55

60

Asp Lys Thr Pro Glu Pro
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<223> FQ118 (Ala13) mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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<223> D120 (Ala14) mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
 20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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 <223> AAA136 (Leu) mutation

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Gly Cys Gln Thr Ser Asn Asp Leu Leu Leu Glu Ala Leu Asn Ala Ser
 20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Ala Ala Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Ala Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Ala Leu Ala Ala Ser
 20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
 50 55 60

Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
 20 25 30

Ser Ala Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Ala Thr Pro Ala Pro
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 Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
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 Ser Ala Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
 35 40 45
 Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
 50 55 60
 Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
 20 25 30

Ser Lys Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
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Ser Lys Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
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Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
          20          25          30

Ser Lys Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
          35          40          45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
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Asp Lys Thr Pro Glu Pro
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
65 70

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<223> L148 mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
65 70

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<223> L148V and L148V* mutations

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser
20 25 30

Ser Lys Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
65 70

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<223> L148G mutation

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20 25 30

Ser Lys Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
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<222> (40)..(41)

<223> III151 mutation

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20 25 30

Ser Lys Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe
50 55 60

Asp Lys Thr Pro Glu Pro
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 <400> 33
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 <223> Mutagenesis oligonucleotide for Q-HN165 (Ala8)

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 gaagccatgg cgccggagtc gcatcaaata tcc 33

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 <211> 37
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 <223> Mutagenesis oligonucleotide for AAA136 (Leu)

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<210> 39
 <211> 54
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 <223> Mutagenesis oligonucleotide for E--N140 + KEE146 (Ala4+5)

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 <223> Mutagenesis oligonucleotide for E145

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 <223> Mutagenesis oligonucleotide for II151

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 <223> TGMV AL1 coding sequence

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 gcccaaagag attggcagac taactgtaaa tacggaaagc cagttcaaat taaaggaggt 900
 atcccgtaa tcgtgctgtg caatcctgga gagggtgcta gctataaagt tttcctcgac 960
 aaagaggaaa aactccact aaagaactgg actttccata atgcgaaatt cgtcttctc 1020
 aactcccccc tctatcaaag ctcaacacag agcagc 1056

<210> 51
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>

<221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 FQ118 mutant (Ala13)

<400> 51

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa gcc gcg gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Ala Ala Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	

tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 52
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 52

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln

50	55	60
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val		
65	70	75 80
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys		
	85	90 95
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu		
	100	105 110
Val Trp Gly Glu Ala Ala Val Asp Gly Arg Ser Ala Arg Gly Gly Cys		
	115	120 125
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys		
	130	135 140
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu		
	145	150 155 160
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys		
	165	170 175
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn		
	180	185 190
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser		
	195	200 205
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp		
	210	215 220
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn		
	225	230 235 240
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys		
	245	250 255
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu		
	260	265 270
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		
	275	280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 53
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 D120 (Ala14) mutant

<400> 53
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

gta tgg gga gaa gcc gcg gtc gcc ggc cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Ala Ala Val Ala Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 54
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 54

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Ala Ala Val Ala Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn

180 185 190
 Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205
 Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220
 Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240
 Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255
 Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270
 Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285
 Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 55
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 RS-R125 (Ala1) mutant

<400> 55
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe

48

1	5	10	15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa				96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	20	25	30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc				144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	35	40	45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag				192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	50	55	60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta				240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	65	70	75	80
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa				288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	85	90	95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt				336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	100	105	110	
gta tgg gga gaa ttc cag gtc gac ggt gcg gcc gct gca gga ggt tgc				384
Val Trp Gly Glu Phe Gln Val Asp Gly Ala Ala Ala Ala Gly Gly Cys	115	120	125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa				432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	130	135	140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta				480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	145	150	155	160
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag				528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	165	170	175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac				576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	180	185	190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt				624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	195	200	205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat				672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	210	215	220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat				720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	225	230	235	240

tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	

gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	

aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	

tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 56
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 56

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Ala Ala Ala Ala Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
305 310 315 320
325 330 335

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<210> 57
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus
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<400>	57															
atg	cca	tcg	cat	cca	aaa	cgg	ttt	caa	ata	aat	gcc	aaa	aat	tat	ttt	48
Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe	
1				5					10					15		
ctt	aca	tat	cct	cag	tgc	tcc	ttg	tcc	aaa	gaa	gaa	tca	ctt	tct	caa	96
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln	
			20					25					30			
tta	caa	gcc	cta	aac	act	cgg	att	aac	aaa	aaa	ttc	ata	aaa	atc	tgc	144
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	
		35					40					45				
aga	gag	ctt	cat	gaa	gat	ggg	caa	cct	cac	ctc	cac	gtg	ctt	att	cag	192
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln	
	50					55					60					
ttc	gag	gga	aaa	tac	tgc	tgc	caa	aat	caa	cga	ttc	ttc	gac	ctg	gta	240
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val	
65				70					75					80		
tcc	cca	aca	agg	tca	gca	cat	ttc	cat	cca	aac	att	cag	aga	gct	aaa	288
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys	
				85					90					95		
tcg	tct	tcc	gac	gtc	aag	acg	tac	atc	gac	aaa	gac	gga	gat	act	ctt	336
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu	
			100					105					110			
gta	tgg	gga	gaa	ttc	cag	gtc	gac	ggg	cga	agt	gct	aga	gga	ggg	tgc	384
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys	
		115					120					125				
gca	gct	agc	aac	gac	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa	432
Ala	Ala	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys	

130	135	140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta			480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu			
145	150	155	160
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag			528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys			
	165	170	175
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac			576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn			
	180	185	190
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt			624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser			
	195	200	205
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat			672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp			
	210	215	220
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat			720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			
	225	230	235
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag			768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys			
	245	250	255
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg			816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu			
	260	265	270
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac			864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
	275	280	285
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc			912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
	290	295	300
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac			960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
	305	310	315
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa			1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
	325	330	335
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc			1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
	340	345	350

<210> 58
<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 58

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Ala Ala Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220
 Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240
 Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255
 Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270
 Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285
 Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 59
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 ND133 (Ala3) mutant

<400> 59
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144

Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys		
		35					40					45					
aga	gag	ctt	cat	gaa	gat	ggg	caa	cct	cac	ctc	cac	gtg	ctt	att	cag	192	
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln		
	50					55				60							
ttc	gag	gga	aaa	tac	tgc	tgc	caa	aat	caa	cga	ttc	ttc	gac	ctg	gta	240	
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val		
65				70						75				80			
tcc	cca	aca	agg	tca	gca	cat	ttc	cat	cca	aac	att	cag	aga	gct	aaa	288	
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys		
			85						90					95			
tcg	tct	tcc	gac	gtc	aag	acg	tac	atc	gac	aaa	gac	gga	gat	act	ctt	336	
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu		
			100					105					110				
gta	tgg	gga	gaa	ttc	cag	gtc	gac	ggt	cga	agt	gct	aga	gga	ggt	tgc	384	
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys		
	115						120					125					
caa	aca	tct	gcg	gcc	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa	432	
Gln	Thr	Ser	Ala	Ala	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys		
	130					135					140						
gaa	gaa	gcc	ctg	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta	480	
Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu		
145				150						155					160		
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528	
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys		
				165					170					175			
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576	
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn		
			180					185					190				
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624	
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser		
	195						200					205					
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672	
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp		
	210					215					220						
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720	
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn		
225				230						235					240		
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768	
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys		
				245				250						255			
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816	
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu		

260	265	270	
aaa cat tgg aaa gaa ctc att	ggg gcc caa aga gat tgg	cag act aac	864
Lys His Trp Lys Glu Leu Ile	Gly Ala Gln Arg Asp Trp	Gln Thr Asn	
275	280	285	
tgt aaa tac gga aag cca gtt	caa att aaa gga ggt atc	ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val	Gln Ile Lys Gly Gly Ile	Pro Ser Ile	
290	295	300	
gtg ctg tgc aat cct gga gag	ggt gct agc tat aaa gtt	ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu	Gly Ala Ser Tyr Lys Val	Phe Leu Asp	
305	310	315 320	
aaa gag gaa aac act cca cta	aag aac tgg act ttc cat	aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu	Lys Asn Trp Thr Phe His	Asn Ala Lys	
325	330	335	
ttc gtc ttc ctc aac tcc ccc	ctc tat caa agc tca aca	cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro	Leu Tyr Gln Ser Ser Thr	Gln Ser Ser	
340	345	350	
<210> 60			
<211> 352			
<212> PRT			
<213> Tomato golden mosaic virus			
<400> 60			
Met Pro Ser His Pro Lys Arg	Phe Gln Ile Asn Ala Lys	Asn Tyr Phe	
1	5	10 15	
Leu Thr Tyr Pro Gln Cys Ser	Leu Ser Lys Glu Glu Ser	Leu Ser Gln	
20	25	30	
Leu Gln Ala Leu Asn Thr Pro	Ile Asn Lys Lys Phe Ile	Lys Ile Cys	
35	40	45	
Arg Glu Leu His Glu Asp Gly	Gln Pro His Leu His Val	Leu Ile Gln	
50	55	60	
Phe Glu Gly Lys Tyr Cys Cys	Gln Asn Gln Arg Phe Phe	Asp Leu Val	
65	70	75 80	
Ser Pro Thr Arg Ser Ala His	Phe His Pro Asn Ile Gln	Arg Ala Lys	
85	90	95	
Ser Ser Ser Asp Val Lys Thr	Tyr Ile Asp Lys Asp Gly	Asp Thr Leu	
100	105	110	

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Ala Ala Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 61
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 E--N140 (Ala4) mutant

<400> 61
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125
 caa aca tct aac gac gct gca gcg gcc gcg tta gct gct tct tcc aaa 432
 Gln Thr Ser Asn Asp Ala Ala Ala Ala Leu Ala Ala Ser Ser Lys
 130 135 140
 gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480
 Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160
 ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528

Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
				165					170					175		
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
			180					185					190			
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
		195					200					205				
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
	210					215					220					
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225					230				235						240	
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
				245				250						255		
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
			260					265					270			
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
		275					280					285				
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggg	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
	290					295					300					
gtg	ctg	tgc	aat	cct	gga	gag	ggg	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310				315						320	
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
				325				330						335		
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
			340					345					350			

<210> 62
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 62

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 63
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 KEE146 (Ala5) mutant

<400> 63
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc gcg	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala	
130 135 140	
gcc gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac 960
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa 1008
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 64
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 64

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala
 130 135 140

Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 65
 <211> 1056
 <212> DNA

<213> Tomato golden mosaic virus

<220>

<221> CDS

<222> (1)..(1056)

<223> TGMV AL1 REK154 (Ala6) mutant

<400> 65

atg cca tgc cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	

gaa gaa gcc ctg cag ata att gcg gcc gca atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Ala Ala Ala Ile Pro Glu Lys Tyr Leu	
145 150 155 160	

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 66
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 66

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys

35	40	45
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln 50 55 60		
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80		
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95		
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu 100 105 110		
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125		
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140		
Glu Glu Ala Leu Gln Ile Ile Ala Ala Ala Ile Pro Glu Lys Tyr Leu 145 150 155 160		
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175		
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190		
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205		
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp 210 215 220		
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240		
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255		
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270		

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 67
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 EKY159 (Ala7) mutant

<400> 67
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gcg gcc gct tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala Ala Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 68
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus
 <400> 68

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala Ala Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys

				165						170						175
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
			180					185					190			
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
		195					200					205				
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
	210					215					220					
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225					230					235					240	
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
				245					250					255		
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
			260					265					270			
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
		275					280					285				
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
	290					295					300					
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310					315					320	
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
				325					330					335		
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
			340					345					350			

<210> 69
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 Q-HN165 (Ala8) mutant

<400> 69

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt gcg ttc gcc gct cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	

agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 70
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 70

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile

290		295		300	
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp					
305		310		315	320
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys					
		325		330	335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser					
		340		345	350
<210> 71					
<211> 1056					
<212> DNA					
<213> Tomato golden mosaic virus					
<220>					
<221> CDS					
<222> (1)..(1056)					
<223> TGMV AL1 N-DR172 (Ala9) mutant					
<400> 71					
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt					48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe					
1		5		10	15
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa					96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln					
		20		25	30
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc					144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys					
		35		40	45
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag					192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln					
		50		55	60
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta					240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val					
65		70		75	80
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa					288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys					
		85		90	95
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt					336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu					
		100		105	110
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc					384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys					

115	120	125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140			432
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160			480
ttt cag ttc cac aat cta aat agc gcg cta gct gcg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe Asp Lys 165 170 175			528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190			576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205			624
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp 210 215 220			672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240			720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255			768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270			816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285			864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile 290 295 300			912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305 310 315 320			960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325 330 335			1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser 340 345 350			1056

<210> 72
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 72

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 73
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 K--E179 (Ala10) mutant

<400> 73
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96

Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln		
			20					25					30				
tta	caa	gcc	cta	aac	act	ccg	att	aac	aaa	aaa	ttc	ata	aaa	atc	tgc		144
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys		
		35					40					45					
aga	gag	ctt	cat	gaa	gat	ggg	caa	cct	cac	ctc	cac	gtg	ctt	att	cag		192
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln		
	50					55					60						
ttc	gag	gga	aaa	tac	tgc	tgc	caa	aat	caa	cga	ttc	ttc	gac	ctg	gta		240
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val		
65					70					75					80		
tcc	cca	aca	agg	tca	gca	cat	ttc	cat	cca	aac	att	cag	aga	gct	aaa		288
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys		
				85					90					95			
tcg	tct	tcc	gac	gtc	aag	acg	tac	atc	gac	aaa	gac	gga	gat	act	ctt		336
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu		
			100					105					110				
gta	tgg	gga	gaa	ttc	cag	gtc	gac	ggt	cga	agt	gct	aga	gga	ggt	tgc		384
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys		
		115					120					125					
caa	aca	tct	aac	gac	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa		432
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys		
		130				135					140						
gaa	gaa	gcc	ctg	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta		480
Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu		
145					150					155					160		
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	gcg		528
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Ala		
				165					170					175			
act	ccg	gcg	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac		576
Thr	Pro	Ala	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn		
			180					185					190				
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt		624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr		Phe	Gly	Lys	Ser	
		195					200					205					
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat		672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp		
		210				215					220						
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat		720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn		
225					230					235					240		
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag		768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys		

245										250										255										
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg		816													
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu															
			260					265					270																	
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac		864													
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn															
		275					280					285																		
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggg	atc	ccg	tca	atc		912													
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile															
	290					295					300																			
gtg	ctg	tgc	aat	cct	gga	gag	ggg	gct	agc	tat	aaa	gtt	ttc	ctc	gac		960													
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp															
305					310				315					320																
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa		1008													
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys															
			325					330					335																	
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc		1056													
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser															
			340				345					350																		

<210> 74
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

 <400> 74

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln
			20					25					30		
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
		35					40					45			
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln
	50					55					60				
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val
65					70					75				80	
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys
				85					90					95	

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Ala
 165 170 175

Thr Pro Ala Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 75
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 AAA136 (Leu) mutant

<400> 75
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125
 caa aca tct aac gac ctt cta cta gag gcc tta aat gct tct tcc aaa 432
 Gln Thr Ser Asn Asp Leu Leu Leu Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140
 gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480

Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	
145					150					155					160	
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
				165					170					175		
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
			180					185					190			
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
		195					200					205				
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
	210					215					220					
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225					230				235						240	
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
				245					250					255		
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
			260					265					270			
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
		275					280					285				
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
	290					295					300					
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310				315						320	
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
				325					330					335		
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
			340					345					350			

<210> 76
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 76

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Leu Leu Leu Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 77
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 E--N140 + KEE146 (Ala4+5) mutant

<400> 77
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gcg gcc gcg tta gct gct tct tcc gcg	432
Gln Thr Ser Asn Asp Ala Ala Ala Ala Leu Ala Ala Ser Ser Ala	
130 135 140	
gcc gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864

Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn		
		275					280					285					
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggg	atc	ccg	tca	atc	912	
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile		
	290					295				300							
gtg	ctg	tgc	aat	cct	gga	gag	ggg	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960	
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp		
305					310				315					320			
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008	
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys		
			325					330					335				
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056	
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser		
			340					345					350				
<210> 78																	
<211> 352																	
<212> PRT																	
<213> Tomato golden mosaic virus																	
<400> 78																	
Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe		
1				5					10					15			
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln		
			20					25					30				
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys		
	35						40					45					
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln		
	50					55					60						
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val		
65					70					75				80			
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys		
				85					90					95			
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu		
			100					105					110				
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys		
		115					120					125					

Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser Ser Ala
 130 135 140

Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 79
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 K144 mutant

<400> 79
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125
 caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc gcg 432
 Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala
 130 135 140
 gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480
 Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160
 ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528
 Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 80
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 80

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln

	20		25		30														
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys				
	35						40					45							
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln				
	50					55					60								
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val				
65					70					75					80				
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys				
				85					90					95					
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu				
			100					105					110						
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys				
		115					120					125							
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Ala				
	130					135					140								
Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu				
145					150					155					160				
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys				
				165					170					175					
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn				
			180					185						190					
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser				
		195					200					205							
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp				
	210					215					220								
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn				
225					230					235					240				
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys				
				245					250					255					

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 81
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 E145 mutant

<400> 81
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gca gag gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac 960
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa 1008
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 82
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 82

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu

145		150		155		160
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys						
		165		170		175
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn						
		180		185		190
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser						
		195		200		205
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp						
		210		215		220
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn						
		225		230		235
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys						
		245		250		255
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu						
		260		265		270
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn						
		275		280		285
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile						
		290		295		300
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp						
		305		310		315
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys						
		325		330		335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser						
		340		345		350

<210> 83
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

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<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 E146 mutant

<400> 83
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt      48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1          5          10          15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa      96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
          20          25          30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc      144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
          35          40          45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag      192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
          50          55          60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta      240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65          70          75          80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa      288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
          85          90          95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt      336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
          100          105          110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc      384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
          115          120          125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa      432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
          130          135          140

gaa gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta      480
Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145          150          155          160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag      528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
          165          170          175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac      576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
          180          185          190

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt      624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
          195          200          205

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tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 84
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 84

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn

275	280	285
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		
290	295	300
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		
305	310	315
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		
325	330	335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		
340	345	350

<210> 85
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 EE146 mutant

<400> 85	
atg cca tgc cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	

100										105										110										
gta	tgg	gga	gaa	ttc	cag	gtc	gac	ggg	cga	agt	gct	aga	gga	ggg	tgc	384														
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys															
115					120					125																				
caa	aca	tct	aac	gac	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa	432														
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys															
130					135					140																				
gcg	gcc	gcc	ctg	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta	480														
Ala	Ala	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu															
145					150					155					160															
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528														
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys															
165					170					175																				
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576														
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn															
180					185					190																				
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624														
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser															
195					200					205																				
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672														
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp															
210					215					220																				
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720														
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn															
225					230					235					240															
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768														
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys															
245					250					255																				
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816														
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu															
260					265					270																				
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864														
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn															
275					280					285																				
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggg	atc	ccg	tca	atc	912														
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile															
290					295					300																				
gtg	ctg	tgc	aat	cct	gga	gag	ggg	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960														
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp															
305					310					315					320															
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008														
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys															
325					330					335																				

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 86
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 86

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 87
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 A147Y mutant

<400> 87
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt

48

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe		
1				5					10					15			
ctt	aca	tat	cct	cag	tgc	tcc	ttg	tcc	aaa	gaa	gaa	tca	ctt	tct	caa		96
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln		
			20					25					30				
tta	caa	gcc	cta	aac	act	ccg	att	aac	aaa	aaa	ttc	ata	aaa	atc	tgc		144
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys		
		35					40					45					
aga	gag	ctt	cat	gaa	gat	ggg	caa	cct	cac	ctc	cac	gtg	ctt	att	cag		192
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln		
	50					55					60						
ttc	gag	gga	aaa	tac	tgc	tgc	caa	aat	caa	cga	ttc	ttc	gac	ctg	gta		240
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val		
65					70				75					80			
tcc	cca	aca	agg	tca	gca	cat	ttc	cat	cca	aac	att	cag	aga	gct	aaa		288
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys		
				85					90					95			
tcg	tct	tcc	gac	gtc	aag	acg	tac	atc	gac	aaa	gac	gga	gat	act	ctt		336
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu		
			100					105					110				
gta	tgg	gga	gaa	ttc	cag	gtc	gac	ggg	cga	agt	gct	aga	gga	ggg	tgc		384
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys		
		115					120					125					
caa	aca	tct	aac	gac	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa		432
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys		
		130					135				140						
gaa	gaa	tac	ctt	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta		480
Glu	Glu	Tyr	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu		
145					150				155						160		
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag		528
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys		
				165				170						175			
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac		576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn		
			180					185					190				
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt		624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser		
		195					200					205					
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat		672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp		
		210				215					220						
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat		720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn		

225	230	235	240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag				768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys				
	245	250	255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg				816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu				
	260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac				864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn				
	275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc				912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile				
	290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac				960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp				
	305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa				1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys				
	325	330	335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc				1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser				
	340	345	350	

<210> 88
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

 <400> 88

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 89
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 L148 mutant

<400> 89
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125
 caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gct gcg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 90

<211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 90

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 91
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 L148V mutant

<400> 91
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys 35 40 45	144
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln 50 55 60	192
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80	240
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95	288
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu 100 105 110	336
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140	432
gaa gag gcc gtg cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255	768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816

Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu		
			260					265					270				
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864	
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn		
		275					280					285					
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912	
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile		
	290					295					300						
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960	
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp		
305					310				315						320		
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008	
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys		
			325					330						335			
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056	
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser		
		340					345						350				
<210>		92															
<211>		352															
<212>		PRT															
<213>		Tomato golden mosaic virus															
<400>		92															
Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe		
1				5					10					15			
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln		
			20					25					30				
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys		
		35					40					45					
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln		
	50					55					60						
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val		
65					70				75					80			
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys		
				85					90					95			
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu		
			100					105					110				

Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys	115	120	125
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys	130	135	140
Glu	Glu	Ala	Val	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	145	150	155
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	165	170	175
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	180	185	190
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	195	200	205
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	210	215	220
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	225	230	235
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	245	250	255
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	260	265	270
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	275	280	285
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	290	295	300
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	305	310	315
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	325	330	335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 93
 <211> 1056
 <212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 L148V* mutant

<400> 93
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125
 caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432
 Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140
 gaa gaa gcc gtt cag ata att aga gag aaa atc cca gaa aaa tat tta 480
 Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 94
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 94

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe

1	5	10	15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	20	25	30
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	35	40	45
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	50	55	60
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	65	70	75
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	85	90	95
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	100	105	110
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	115	120	125
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	130	135	140
Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	145	150	155
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	165	170	175
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	180	185	190
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	195	200	205
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	210	215	220
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	225	230	235
			240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
340 345 350

<210> 95
<211> 1056
<212> DNA
<213> Tomato golden mosaic virus

<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 L148G mutant

<400> 95
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ggc cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	

tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc 912
 Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile
 290 295 300

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac 960
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp
 305 310 315 320

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa 1008
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys
 325 330 335

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser
 340 345 350

<210> 96
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 96

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys

130	135	140															
Glu	Glu	Ala	Gly	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu		
145					150					155					160		
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys		
				165					170					175			
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn		
			180					185					190				
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser		
		195					200					205					
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp		
210						215					220						
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn		
225					230					235					240		
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys		
				245					250					255			
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu		
			260					265					270				
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn		
		275					280					285					
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile		
		290				295					300						
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp		
305					310					315					320		
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys		
				325					330					335			
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser		
			340					345					350				

<210> 97
 <211> 1056

<212> DNA
 <213> Tomato golden mosaic virus

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> TGMV AL1 III151 mutant

<400> 97
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
 1 5 10 15
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
 20 25 30
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125
 caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432
 Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140
 gaa gaa gcc ctt cag gca gct aga gag aaa atc cca gaa aaa tat tta 480
 Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160
 ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528
 Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175
 act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac 576
 Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 98
 <211> 352
 <212> PRT
 <213> Tomato golden mosaic virus

<400> 98

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
 130 135 140

Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys Tyr Leu
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu

Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro
1 5 10

<210> 101
<211> 13
<212> PRT
<213> tomato yellow leaf curl virus

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> TYLCV C1 amino acids 142-154

<400> 101

Lys Ser Glu Ala Leu Lys Ile Leu Arg Glu Leu Ala Pro
1 5 10

<210> 102
<211> 13
<212> PRT
<213> cabbage leaf curl virus

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> CbLCV AL1 amino acids 141-153

<400> 102

Val Glu Glu Ala Leu Ala Ile Ile Arg Ala Gly Asp Pro
1 5 10

<210> 103
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide primer

<400> 103
ggacaccgat tggatccagc atgcctc

27

<210> 104
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide primer

<400> 104
ccacagtcga attccccggg cttacgc 27

<210> 105
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Mutagenesis oligonucleotide

<400> 105
cctaaataag atctacaagg atcccacgaa acccta 36

<210> 106
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> CbLCV AL1 L145A mutagenesis oligonucleotide

<400> 106
gtgtggaaga ggcggccgca attataaggg c 31

<210> 107
<211> 349
<212> PRT
<213> cabbage leaf curl virus

<400> 107

Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met
20 25 30

Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val
35 40 45

Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile
50 55 60

Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile
65 70 75 80

Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala

85

90

95

Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr
 100 105 110

Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys
 115 120 125

Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala
 130 135 140

Leu Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr
 145 150 155 160

His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu
 165 170 175

Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp
 180 185 190

Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala
 195 200 205

Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr
 210 215 220

Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser
 225 230 235 240

Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr
 245 250 255

Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp
 260 265 270

Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr
 275 280 285

Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys
 290 295 300

Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu
 305 310 315 320

Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr
325 330 335

Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys
340 345

<210> 108
<211> 70
<212> PRT
<213> cabbage leaf curl virus

<220>
<221> MISC_FEATURE
<222> (1)..(70)
<223> Wild-type CbLCV AL1 amino acids 111-180

<400> 108

Asp Tyr Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala
1 5 10 15

Asn Lys Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu
20 25 30

Glu Ala Leu Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val
35 40 45

Ser Tyr His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala
50 55 60

Pro Glu Pro Trp Ala Pro
65 70

<210> 109
<211> 70
<212> PRT
<213> cabbage leaf curl virus

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> L145A mutation

<400> 109

Asp Tyr Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala

1					5					10					15				
Asn	Lys	Asp	Asp	Val	Tyr	His	Asn	Ala	Val	Asn	Ala	Gly	Cys	Val	Glu				
			20				25						30						
.																			
Glu	Ala	Ala	Ala	Ile	Ile	Arg	Ala	Gly	Asp	Pro	Lys	Thr	Phe	Ile	Val				
			35				40						45						
.																			
Ser	Tyr	His	Asn	Val	Arg	Ala	Asn	Ile	Glu	Arg	Leu	Phe	Thr	Lys	Ala				
			50				55						60						
.																			
Pro	Glu	Pro	Trp	Ala	Pro														
65				70															

gacatagctc cgcattatct aaagctaaag cactggaaaag agcttattgg ggcccaaagg 840
gactggcaat caaactgtaa gtacggcaag ccagttcaaa ttaaagggtgg cataccctca 900
atcgtgctgt gcaatccagg agaggggagc agttatataa gtttcctcaa caaagaggaa 960
aatgcatcac taagagcgtg gactaccaa aatgcaaaat tcatcactct tgaagccccc 1020
ctctatcaaa gcacagcaca agattgc 1047

<210> 111
<211> 1047
<212> DNA
<213> cabbage leaf curl virus

<220>
<221> CDS
<222> (1)..(1047)
<223> CbLCV AL1 L145A mutation

<400> 111
atg cca cga aac cct aaa tcg ttt cgt tta gca gcc cga aat ata ttc 48
Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe
1 5 10 15
tta aca tat ccc cag tgc gac ata ccc aaa gat gaa gct ctt cag atg 96
Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met
20 25 30
ctt caa acc ctg tcg tgg tca gtc gtc aaa ccc aca tac atc aga gtc 144
Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val
35 40 45
gca aga gag gaa cat tca gac ggg ttc ccc cat tta cac tgt ctc atc 192
Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile
50 55 60
caa cta tca gga aag tcg aac atc aag gat gct aga ttt ttc gac atc 240
Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile
65 70 75 80
act cac ccc aga agg tct gcc aat ttt cac cca aac att cag gca gcc 288
Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala
85 90 95
aaa gac acc aat gcc gtc aag aat tac atc acc aaa gat ggt gat tat 336
Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr
100 105 110
tgt gaa tcc ggg cag tac aag gtg tct ggg ggt aca aag gca aat aaa 384
Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys
115 120 125
gac gac gtc tac cac aac gcc gtc aat gcg gga tgt gtg gaa gag gcg 432
Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala

130	135	140	
gcc gca att ata agg gct gga gat cca aag acg ttc att gtt agt tat Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr 145 150 155 160			480
cat aat gtt aga gct aac ata gag cga ctc ttt act aag gct ccg gaa His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu 165 170 175			528
cca tgg gct cct ccg ttt caa ctc tcc tcc ttt act aac gtc ccg gac Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp 180 185 190			576
gag atg agt tca tgg gca gat gac tat ttt ggt cgg agt gcc gct gcg Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala 195 200 205			624
cgg gcg gaa aga cct att agt atc ata gtt gaa ggt gat tca cga acc Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr 210 215 220			672
ggc aag acc atg tgg gcg cgt gct tta gga cca cat aat tat ttg agt Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser 225 230 235 240			720
ggg cac ctc gac ttt aat tca aag gtc ttt tca aat aat gcg gag tat Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr 245 250 255			768
aac gtc att gat gac ata gct ccg cat tat cta aag cta aag cac tgg Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp 260 265 270			816
aaa gag ctt att ggg gcc caa agg gac tgg caa tca aac tgt aag tac Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr 275 280 285			864
ggc aag cca gtt caa att aaa ggt ggc ata ccc tca atc gtg ctg tgc Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys 290 295 300			912
aat cca gga gag ggg agc agt tat ata agt ttc ctc aac aaa gag gaa Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu 305 310 315 320			960
aat gca tca cta aga gcg tgg act acc aaa aat gca aaa ttc atc act Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr 325 330 335			1008
ctt gaa gcc ccc ctc tat caa agc aca gca caa gat tgc Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys 340 345			1047

<210> 112

<211> 349

<212> PRT

<213> cabbage leaf curl virus

<400> 112

Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met
20 25 30

Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val
35 40 45

Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile
50 55 60

Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile
65 70 75 80

Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala
85 90 95

Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr
100 105 110

Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys
115 120 125

Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala
130 135 140

Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr
145 150 155 160

His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu
165 170 175

Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp
180 185 190

Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala
195 200 205

Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr
 210 215 220

Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser
 225 230 235 240

Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr
 245 250 255

Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp
 260 265 270

Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr
 275 280 285

Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys
 290 295 300

Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu
 305 310 315 320

Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr
 325 330 335

Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys
 340 345

<210> 113
 <211> 13
 <212> PRT
 <213> Artificial

<220>
 <223> Consensus begomovirus AL1/C1 sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(3)
 <223> Xaa can be any naturally occurring amino acid, but is generally a charged amino acid which is optionally present or absent

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Xaa can be Leu or Met

<220>

<221> misc_feature
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa can be Ile or Val

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa can be Ile or Leu

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa can be Arg or Lys

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa can be Glu or Asp

<220>
<221> misc_feature
<222> (11)..(12)
<223> Xaa can be any naturally occurring amino acid

<400> 113

Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
1 5 10